

1642

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/436,184

DATE: 06/12/2000

TIME: 16:07:18

Input Set : A:\PT.txt

Output Set: N:\CRF3\06122000\I436184.raw

ENTERED

5 <110> APPLICANT: Wands, Jack R.  
 7 de la Monte, Suzanne M.  
 9 Ince, Nedim  
 11 Carlson, Rolf I.  
 15 <120> TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS  
 19 <130> FILE REFERENCE: R.I. Hosp. - Malignant Neoplasms  
 C--> 23 <140> CURRENT APPLICATION NUMBER: US/09/436,184  
 25 <141> CURRENT FILING DATE: 1999-11-08  
 29 <160> NUMBER OF SEQ ID NOS: 7  
 33 <170> SOFTWARE: PatentIn Ver. 2.0  
 37 <210> SEQ ID NO: 1  
 39 <211> LENGTH: 36  
 41 <212> TYPE: PRT  
 43 <213> ORGANISM: Artificial Sequence  
 47 <220> FEATURE:  
 49 <223> OTHER INFORMATION: Description of Artificial Sequence: Consensus  
 51 EGF-like domain  
 55 <220> FEATURE:  
 57 <223> OTHER INFORMATION: Wherein any Xaa may be any amino acid  
 61 <400> SEQUENCE: 1  
 W--> 63 Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa  
 65 1 5 10 15  
 W--> 69 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Cys Xaa Xaa Xaa Xaa  
 71 20 25 30  
 W--> 75 Xaa Xaa Xaa Cys  
 77 35  
 82 <210> SEQ ID NO: 2  
 84 <211> LENGTH: 758  
 86 <212> TYPE: PRT  
 88 <213> ORGANISM: Homo sapiens  
 92 <400> SEQUENCE: 2  
 94 Met Ala Gln Arg Lys Asn Ala Lys Ser Ser Gly Asn Ser Ser Ser Ser  
 96 1 5 10 15  
 100 Gly Ser Gly Ser Gly Ser Thr Ser Ala Gly Ser Ser Ser Pro Gly Ala  
 102 20 25 30  
 106 Arg Arg Glu Thr Lys His Gly Gly His Lys Asn Gly Arg Lys Gly Gly  
 108 35 40 45  
 112 Leu Ser Gly Thr Ser Phe Phe Thr Trp Phe Met Val Ile Ala Leu Leu  
 114 50 55 60  
 118 Gly Val Trp Thr Ser Val Ala Val Val Trp Phe Asp Leu Val Asp Tyr  
 120 65 70 75 80  
 124 Glu Glu Val Leu Gly Lys Leu Gly Ile Tyr Asp Ala Asp Gly Asp Gly  
 126 85 90 95  
 130 Asp Phe Asp Val Asp Asp Ala Lys Val Leu Leu Gly Leu Lys Glu Arg  
 132 100 105 110  
 136 Ser Thr Ser Glu Pro Ala Val Pro Pro Glu Glu Ala Glu Pro His Thr  
 138 115 120 125

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142 Glu Pro Glu Glu Gln Val Pro Val Glu Ala Glu Pro Gln Asn Ile Glu
144      130      135      140
148 Asp Glu Ala Lys Glu Gln Ile Gln Ser Leu Leu His Glu Met Val His
150 145      150      155      160
154 Ala Glu His Val Glu Gly Glu Asp Leu Gln Gln Glu Asp Gly Pro Thr
156      165      170      175
160 Gly Glu Pro Gln Gln Glu Asp Asp Glu Phe Leu Met Ala Thr Asp Val
162      180      185      190
166 Asp Asp Arg Phe Glu Thr Leu Glu Pro Glu Val Ser His Glu Glu Thr
168      195      200      205
172 Glu His Ser Tyr His Val Glu Glu Thr Val Ser Gln Asp Cys Asn Gln
174      210      215      220
178 Asp Met Glu Glu Met Met Ser Glu Gln Glu Asn Pro Asp Ser Ser Glu
180 225      230      235      240
184 Pro Val Val Glu Asp Glu Arg Leu His His Asp Thr Asp Asp Val Thr
186      245      250      255
190 Tyr Gln Val Tyr Glu Glu Gln Ala Val Tyr Glu Pro Leu Glu Asn Glu
192      260      265      270
196 Gly Ile Glu Ile Thr Glu Val Thr Ala Pro Pro Glu Asp Asn Pro Val
198      275      280      285
202 Glu Asp Ser Gln Val Ile Val Glu Glu Val Ser Ile Phe Pro Val Glu
204      290      295      300
208 Glu Gln Gln Glu Val Pro Pro Glu Thr Asn Arg Lys Thr Asp Asp Pro
210 305      310      315      320
214 Glu Gln Lys Ala Lys Val Lys Lys Lys Lys Pro Lys Leu Leu Asn Lys
216      325      330      335
220 Phe Asp Lys Thr Ile Lys Ala Glu Leu Asp Ala Ala Glu Lys Leu Arg
222      340      345      350
226 Lys Arg Gly Lys Ile Glu Glu Ala Val Asn Ala Phe Lys Glu Leu Val
228      355      360      365
232 Arg Lys Tyr Pro Gln Ser Pro Arg Ala Arg Tyr Gly Lys Ala Gln Cys
234      370      375      380
238 Glu Asp Asp Leu Ala Glu Lys Arg Arg Ser Asn Glu Val Leu Arg Gly
240 385      390      395      400
244 Ala Ile Glu Thr Tyr Gln Glu Val Ala Ser Leu Pro Asp Val Pro Ala
246      405      410      415
250 Asp Leu Leu Lys Leu Ser Leu Lys Arg Arg Ser Asp Arg Gln Gln Phe
252      420      425      430
256 Leu Gly His Met Arg Gly Ser Leu Leu Thr Leu Gln Arg Leu Val Gln
258      435      440      445
262 Leu Phe Pro Asn Asp Thr Ser Leu Lys Asn Asp Leu Gly Val Gly Tyr
264      450      455      460
268 Leu Leu Ile Gly Asp Asn Asp Asn Ala Lys Lys Val Tyr Glu Glu Val
270 465      470      475      480
274 Leu Ser Val Thr Pro Asn Asp Gly Phe Ala Lys Val His Tyr Gly Phe
276      485      490      495
280 Ile Leu Lys Ala Gln Asn Lys Ile Ala Glu Ser Ile Pro Tyr Leu Lys
282      500      505      510
286 Glu Gly Ile Glu Ser Gly Asp Pro Gly Thr Asp Asp Gly Arg Phe Tyr

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288          515          520          525
292 Phe His Leu Gly Asp Ala Met Gln Arg Val Gly Asn Lys Glu Ala Tyr
294          530          535          540
298 Lys Trp Tyr Glu Leu Gly His Lys Arg Gly His Phe Ala Ser Val Trp
300 545          550          555          560
304 Gln Arg Ser Leu Tyr Asn Val Asn Gly Leu Lys Ala Gln Pro Trp Trp
306          565          570          575
310 Thr Pro Lys Glu Thr Gly Tyr Thr Glu Leu Val Lys Ser Leu Glu Arg
312          580          585          590
316 Asn Trp Lys Leu Ile Arg Asp Glu Gly Leu Ala Val Met Asp Lys Ala
318          595          600          605
322 Lys Gly Leu Phe Leu Pro Glu Asp Glu Asn Leu Arg Glu Lys Gly Asp
324          610          615          620
328 Trp Ser Gln Phe Thr Leu Trp Gln Gln Gly Arg Arg Asn Glu Asn Ala
330 625          630          635          640
334 Cys Lys Gly Ala Pro Lys Thr Cys Thr Leu Leu Glu Lys Phe Pro Glu
336          645          650          655
340 Thr Thr Gly Cys Arg Arg Gly Gln Ile Lys Tyr Ser Ile Met His Pro
342          660          665          670
346 Gly Thr His Val Trp Pro His Thr Gly Pro Thr Asn Cys Arg Leu Arg
348          675          680          685
352 Met His Leu Gly Leu Val Ile Pro Lys Glu Gly Cys Lys Ile Arg Cys
354          690          695          700
358 Ala Asn Glu Thr Arg Thr Trp Glu Glu Gly Lys Val Leu Ile Phe Asp
360 705          710          715          720
364 Asp Ser Phe Glu His Glu Val Trp Gln Asp Ala Ser Ser Phe Arg Leu
366          725          730          735
370 Ile Phe Ile Val Asp Val Trp His Pro Glu Leu Thr Pro Gln Gln Arg
372          740          745          750
376 Arg Ser Leu Pro Ala Ile
378          755
383 <210> SEQ ID NO: 3
385 <211> LENGTH: 2324
387 <212> TYPE: DNA
389 <213> ORGANISM: Homo sapiens
393 <400> SEQUENCE: 3
395 cggaccgtgc aatggcccag cgtaagaatg ccaagagcag cggcaacagc agcagcagcg 60
397 gctccggcag cggtagcacg agtgcgggca gcagcagccc cggggcccgg agagagacaa 120
399 agcatggagg acacaagaat gggaggaaaag gcggactctc gggaacttca ttcttcacgt 180
401 ggtttatggt gattgcattg ctgggcgtct ggacatctgt agctgtcgtt tggtttgatc 240
403 ttgttgacta tgaggaaagt ctaggaaaac taggaatcta tgatgctgat ggtgatggag 300
405 attttgatgt ggatgatgcc aaagttttat taggacttaa agagagatct acttcagagc 360
407 cagcagtcgc gccagaagag gctgagccac aactgagcc caggagagcag gttcctgtgg 420
409 aggcagaacc ccagaatatc gaagatgaag caaaagaaca aattcagtc cttctccatg 480
411 aaatggtaca cgcagaacat gttgagggag aagacttgca acaagaagat ggaccacag 540
413 gagaaccaca acaagaggat gatgagtttc ttatggcgac tgatgtagat gatagatttg 600
415 agaccctgga acctgaagta tctcatgaag aaaccgagca tagttaccac gtggaagaga 660
417 cagtttcaca agactgtaat caggatatgg aagagatgat gtctgagcag gaaaatccag 720
419 attccagtga accagtagta gaagatgaaa gattgcacca tgatacagat gatgtaacat 780

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421 accaagtcta tgaggaacaa gcagtatatg aacctctaga aaatgaaggg atagaaatca 840
423 cagaagtaac tgctccccct gaggataatc ctgtagaaga ttcacaggta attgtagaag 900
425 aagtaagcat ttttcctgtg gaagaacagc aggaagtacc accagaaaca aatagaaaaa 960
427 cagatgatcc agaacaaaaa gcaaaaagtt agaaaaagaa gcctaaactt ttaaataaat 1020
429 ttgataagac tattaaagct gaacttgatg ctgcagaaaa actccgtaaa aggggaaaaa 1080
431 ttgaggaagc agtgaatgca tttaaagaac tagtacgcaa ataccctcag agtccacgag 1140
433 caagatatgg gaaggcgagc tgtgaggatg atttggctga gaagaggaga agtaatgagg 1200
435 tgctacgtgg agccatcgag acctaccaag aggtggccag cctacctgat gtccctgcag 1260
437 acctgctgaa gctgagtttg aagcgctcgt cagacaggca acaatttcta ggtcatatga 1320
439 gagggttccct gcttacctcg cagagattag ttcaactatt tcccaatgat acttccttaa 1380
441 aaaatgacct tggcgtggga tacctcttga taggagataa tgacaatgca aagaaaagttt 1440
443 atgaagaggt gctgagtggt acacctaatg atggctttgc taaagtccat tatggcttca 1500
445 tcctgaaggg acagaacaaa attgctgaga gcatcccata tttaaaggaa ggaatagaat 1560
447 ccggagatcc tggcactgat gatgggagat tttatttcca cctgggggat gccatgcaga 1620
449 ggggttggaa caaagaggca tataagtggg atgagcttgg gcacaagaga ggacactttg 1680
451 catctgtctg gcaacgctca ctctacaatg tgaatggact gaaagcacag ccttggtgga 1740
453 ccccaaaaga aacgggctac acagagttag taaagtcttt agaaagaaac tggaagttaa 1800
455 tccgagatga aggccttgca gtgatggata aagccaaaag tctcttctg cctgaggatg 1860
457 aaâacctgag ggaââââââ gactggagcc agttcacgct gtggcagcaa ggaââââââ 1920
459 atgââââââ ctgcaâââââ gctcctââââ cctgtacctt actagââââââ ttccccgaga 1980
461 caacaggatg cagaââââââ cagatcââââ attccatcat gcaccccggg actcacgtgt 2040
463 ggccgcacac agggccacac aactgcaggg tccgaatgca cctgggcttg gtgattccca 2100
465 aggaââââââ caââââââââ tgtgccââââ agaccaggac ctgggââââââ ggcaââââââ 2160
467 tcatctttga tgaactcttt gagcacgagg tatggcagga tgcctcatct ttccggctga 2220
469 tattcatcgt ggatgtgtgg catccggaac tgacaccaca gcagagacgc agccttccag 2280
471 caatttagca tgaattcatg caââââââââ aâââââââââ gaga 2324

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474 <210> SEQ ID NO: 4  
 476 <211> LENGTH: 31  
 478 <212> TYPE: PRT  
 480 <213> ORGANISM: Artificial Sequence  
 484 <220> FEATURE:  
 486 <223> OTHER INFORMATION: Description of Artificial Sequence: EGF-like  
 488 cysteine-rich repeat  
 492 <220> FEATURE:  
 494 <223> OTHER INFORMATION: Wherein any Xaa may be any amino acid  
 498 <400> SEQUENCE: 4

500 Cys Asp Xaa Xaa Xaa Cys Xaa Xaa Lys Xaa Gly Asn Gly Xaa Cys Asp  
 502 1 5 10 15  
 506 Xaa Xaa Cys Asn Asn Ala Ala Cys Xaa Xaa Asp Gly Xaa Asp Cys  
 508 20 25 30

513 <210> SEQ ID NO: 5  
 515 <211> LENGTH: 1242  
 517 <212> TYPE: PRT  
 519 <213> ORGANISM: Homo sapiens  
 523 <400> SEQUENCE: 5  
 525 Met Ala Ser Pro Glu Ser Asp Gly Phe Ser Asp Val Arg Lys Val  
 527 1 5 10 15  
 531 Gly Tyr Leu Arg Lys Pro Lys Ser Met His Lys Arg Phe Phe Val Leu  
 533 20 25 30

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537 Arg Ala Ala Ser Glu Ala Gly Gly Pro Ala Arg Leu Glu Tyr Tyr Glu
539      35      40      45
543 Asn Glu Lys Lys Trp Arg His Lys Ser Ser Ala Pro Lys Arg Ser Ile
545      50      55      60
549 Pro Leu Glu Ser Cys Phe Asn Ile Asn Lys Arg Ala Asp Ser Lys Asn
551      65      70      75      80
555 Lys His Leu Val Ala Leu Tyr Thr Arg Asp Glu His Phe Ala Ile Ala
557      85      90      95
561 Ala Asp Ser Glu Ala Glu Gln Asp Ser Trp Tyr Gln Ala Leu Leu Gln
563      100      105      110
567 Leu His Asn Arg Ala Lys Gly His Asp Gly Ala Ala Leu Gly
569      115      120      125
573 Ala Gly Gly Gly Gly Ser Cys Ser Gly Ser Ser Gly Leu Gly Glu
575      130      135      140
579 Ala Gly Glu Asp Leu Ser Tyr Gly Asp Val Pro Pro Gly Pro Ala Phe
581      145      150      155      160
585 Lys Glu Val Trp Gln Val Ile Leu Lys Pro Lys Gly Leu Gly Gln Thr
587      165      170      175
591 Lys Asn Leu Ile Gly Ile Tyr Arg Leu Cys Leu Thr Ser Lys Thr Ile
593      180      185      190
597 Ser Phe Val Lys Leu Asn Ser Glu Ala Ala Val Val Leu Gln Leu
599      195      200      205
603 Met Asn Ile Arg Arg Cys Gly His Ser Glu Asn Phe Phe Ile Glu
605      210      215      220
609 Val Gly Arg Ser Ala Val Thr Gly Pro Gly Glu Phe Trp Met Gln Val
611      225      230      235      240
615 Asp Asp Ser Val Val Ala Gln Asn Met His Glu Thr Ile Leu Glu Ala
617      245      250      255
621 Met Arg Ala Met Ser Asp Glu Phe Arg Pro Arg Ser Lys Ser Gln Ser
623      260      265      270
627 Ser Ser Asn Cys Ser Asn Pro Ile Ser Val Pro Leu Arg Arg His His
629      275      280      285
633 Leu Asn Asn Pro Pro Pro Ser Gln Val Gly Leu Thr Arg Arg Ser Arg
635      290      295      300
639 Thr Glu Ser Ile Thr Ala Thr Ser Pro Ala Ser Met Val Gly Gly Lys
641      305      310      315      320
645 Pro Gly Ser Phe Arg Val Arg Ala Ser Ser Asp Gly Glu Gly Thr Met
647      325      330      335
651 Ser Arg Pro Ala Ser Val Asp Gly Ser Pro Val Ser Pro Ser Thr Asn
653      340      345      350
657 Arg Thr His Ala His Arg His Arg Gly Ser Ala Arg Leu His Pro Pro
659      355      360      365
663 Leu Asn His Ser Arg Ser Ile Pro Met Pro Ala Ser Arg Cys Ser Pro
665      370      375      380
669 Ser Ala Thr Ser Pro Val Ser Leu Ser Ser Ser Thr Ser Gly His
671      385      390      395      400
675 Gly Ser Thr Ser Asp Cys Leu Phe Pro Arg Arg Ser Ser Ala Ser Val
677      405      410      415
681 Ser Gly Ser Pro Ser Asp Gly Gly Phe Ile Ser Ser Asp Glu Tyr Gly

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## VERIFICATION SUMMARY

DATE: 06/12/2000

PATENT APPLICATION: US/09/436,184

TIME: 16:07:19

Input Set : A:\PT.txt

Output Set: N:\CRF3\06122000\I436184.raw

L:23 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:63 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1  
L:63 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1  
L:63 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:1  
L:69 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1  
L:69 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1  
M:340 Repeated in SeqNo=1  
L:75 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1  
L:75 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1  
L:500 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4  
L:500 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4  
L:500 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:4  
L:506 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4  
L:506 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4  
M:340 Repeated in SeqNo=4